

**Population structure of wild musk shrews (*Suncus murinus*) in Asia based on mitochondrial DNA variation, with research in Cambodia and Bhutan.**

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The musk shrew (*Suncus murinus*) is a small mammalian species belonging to Insectivora. It is widely distributed in Asia. To identify the genetic relationship among wild musk shrew populations and examine its migration route, we investigated the populations of Cambodia and Bhutan by using mitochondrial DNA restriction fragment length polymorphism analysis and compared them with other Asian populations previously described. Four haplotypes were detected in Cambodia and eight in Bhutan. A total of 53 haplotypes were detected in Asia and were classified largely into two groups, the Continental and Island types, based on a minimum spanning network. From the distribution of mtDNA types in wild musk shrews, three major population groups are identified in Asia: South Asia, Southeast Asia, and Malay. It is suggested that the Malay population group was a mix of South and Southeast Asian population groups and that this was a contact area of the two groups. In addition, other contact areas between the South and Southeast Asian groups exist in Myanmar, but unlike the Malay, the Myanmar area was the border of these groups.

PMID: 17318375 [PubMed - indexed for MEDLINE]

**Phylogeography of wild musk shrew (*Suncus murinus*) populations in Asia based on blood protein/enzyme variation.**

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The musk shrew (*Suncus murinus*) is an insectivore species that inhabits tropical and subtropical Asia widely. To clarify the genetic relationship among wild musk shrew populations, we examined the electrophoretic variants of biparentally inherited genetic markers at 10 loci coding for eight blood proteins/enzymes in a total of 639 animals and compared the results obtained from the mitochondrial DNA data. The principal-component analysis performed using the allele frequency data revealed that the 17 populations could be divided into two major groups, a South Asian group and a Southeast Asian group that includes several island populations bound by Myanmar. The degrees of genetic divergence among populations were higher within the Southeast Asian group than within the South Asian group. This finding was incongruent with the mtDNA diversity. Analysis conducted at the individual level showed that a shrew from the central region in Myanmar that carries a South Asian type of mtDNA showed the electrophoretic variants specific to the Southeast Asian group, suggesting that this region is a contact zone between the two major groups.

PMID: 17551826 [PubMed - indexed for MEDLINE]

## The novel polymorphism of the beta 3-adrenergic receptor gene and its distribution in domestic pigs and wild boars in Asia

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**Source:** [Animal Science Journal](#), Volume 78, Number 3, June 2007 , pp. 243-250(8)

**Publisher:** [Blackwell Publishing](#)

### Abstract:

The beta 3-adrenergic receptor (*ADRB3*) is a G protein-coupled receptor that is involved in regulating energy homeostasis. We have studied DNA sequences of porcine *ADRB3* to find candidate genetic polymorphisms for economically important growth and performance traits in pigs. Five novel haplotypes derived from the three In/dels and 44 SNPs were identified among domestic pigs and wild boars. Three of them encode non-synonymous amino acid sequences by five missense polymorphisms and a frameshift by a thymine insertion. The amino acid polymorphic sites were distributed as follows: one substitution was in extracellular loop 1, three substitutions were in intracellular loop3 and one substitution and the deletion of two amino acids were at the carboxyl-terminal. There was no polymorphism in the transmembrane domains. In addition, we surveyed the allelic frequency of the thymine insertion that cause frameshift in South-east Asian local pigs, including some commercial breeds and wild boars. This thymine insertion was distributed widely in the domestic pigs and wild boars. The frequencies of this allele were relatively low in Western improved breeds, while they were very common in Asian breeds and wild boars in Asia. This result indicates that this insertion originally occurred in ancient Asian wild boars and then circulated among Asian domestic pigs. This allele also spread over Western breeds, probably through the introgression of Asian pigs into European stocks during the 18th and 19th centuries.

**Keywords:** [ADRB3](#); [beta 3-adrenergic receptor](#); [pig](#); [polymorphism](#); [wild boar](#)

**Document Type:** Research article

**DOI:** 10.1111/j.1740-0929.2007.00431.x

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## **Mitochondrial diversity of native pigs in the mainland South and South-east Asian countries and its relationships between local wild boars**

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**Source:** [Animal Science Journal](#), Volume 79, Number 4, August 2008 , pp. 417-434(18)

**Publisher:** [Blackwell Publishing](#)

### **Abstract:**

In this study, we analyzed DNA sequence of mitochondrial DNA (mtDNA) control regions on the 130 native domestic pigs and eight wild boars in the mainland South and South-east Asian countries including Bhutan, Cambodia, Laos, Myanmar, and Vietnam. Forty-four haplotypes were found in the 138 individuals, 41 were in the domestic and four were in wild boars. Only one haplotype was shared by domestic and wild population in Bhutan. In other cases, mtDNA of wild boars did not show close affinity to that of the domestic pigs in the same location, indicating that the native domestic pigs in these countries did not originate in the present habitat. Phylogenetic analyzes of mtDNA haplotypes recapitulated several major clusters identified in other studies, but 11 haplotypes were grouped in a new cluster we named MTSEA. In most cases, more than one lineage group were present in a sampling station, indicating that the present indigenous domestic pigs may have multiple origins. The MTSEA haplotypes were present in relatively high frequencies in domestic pigs in the mountainous area of mainland South-east Asia (Cambodia and Laos), with a few found in Myanmar and Bhutan. The distributions of MTSEA haplotypes are in great conformity with the distribution of present-day Mon-Khmer language and indicated the existence of yet another independent domestication. The D2 haplotypes that distribute high frequency (almost 100%) throughout the Chinese breeds were dominant in Bhutan, Myanmar, and Vietnam. These results suggest an existence of human-mediated dispersal of domestic pigs from north to the south during the historical expansion of Sino-Tibetan and Tai peoples. The D3 haplotypes previously reported in north India were found in sympatric domestic and wild pigs in Bhutan. The D3 haplotype is an important proof of independent domestication event and/or great gene flow between wild and domestic pigs in the foot of Himalaya.

**Keywords:** [human-mediated dispersal](#); [Mainland South and South-east Asia](#); [mitochondrial DNA control region](#); [Mon-Khmer](#); [pig](#)

**Document Type:** Research article

**DOI:** 10.1111/j.1740-0929.2008.00546.x

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